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RAW SEQUENCE LISTING

DATE: 05/31/2002

PATENT APPLICATION: US/10/006,760

TIME: 08:32:21

Input Set : A:\U609011.app

Output Set: N:\CRF3\05312002\J006760.raw

Pb

ENTERED

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3 <110> APPLICANT: Koide, Shohei
5 <120> TITLE OF INVENTION: METHOD OF IDENTIFYING POLYPEPTIDE MONOBODIES WHICH BIND
6   TO TARGET PROTEINS AND USE THEREOF
8 <130> FILE REFERENCE: 176/60901
10 <140> CURRENT APPLICATION NUMBER: 10/006,760
11 <141> CURRENT FILING DATE: 2001-11-19
13 <150> PRIOR APPLICATION NUMBER: 60/249,756
14 <151> PRIOR FILING DATE: 2000-11-17
16 <160> NUMBER OF SEQ ID NOS: 73
18 <170> SOFTWARE: PatentIn Ver. 2.1
20 <210> SEQ ID NO: 1
21 <211> LENGTH: 308
22 <212> TYPE: DNA
23 <213> ORGANISM: Homo sapiens
25 <400> SEQUENCE: 1
26 catatgcagg tttctgatgt tccgcgtgac ctggaagttg ttgctgcgac cccgactagc 60
27 ctgctgatca gctgggatgc tctgcagtt accgtgcggtt attaccgtat cacgtacggt 120
28 gaaaccggtg gtaactcccc gggttcaggaa ttcactgtac ctggttccaa gtctactgct 180
29 accatcagcg gcctgaaacc gggtgtcgac tataccatca ctgtatacgc tgttactggc 240
30 cgtggtgaca gccacgcgag ctccaagcca atctcgatta actaccgtac ctagtaactc 300
31 gaggatcc
34 <210> SEQ ID NO: 2
35 <211> LENGTH: 96
36 <212> TYPE: PRT
37 <213> ORGANISM: Homo sapiens
39 <400> SEQUENCE: 2
40 Met Gln Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr
41   1           5           10           15
43 Pro Thr Ser Leu Leu Ile Ser Trp Asp Ala Pro Ala Val Thr Val Arg
44           20           25           30
46 Tyr Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln
47           35           40           45
49 Glu Phe Thr Val Pro Gly Ser Lys Ser Thr Ala Thr Ile Ser Gly Leu
50           50           55           60
52 Lys Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Thr Gly Arg
53   65           70           75           80
55 Gly Asp Ser Pro Ala Ser Ser Lys Pro Ile Ser Ile Asn Tyr Arg Thr
56           85           90           95
62 <210> SEQ ID NO: 3
63 <211> LENGTH: 96
64 <212> TYPE: PRT
65 <213> ORGANISM: Artificial Sequence
67 <220> FEATURE:

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68 <223> OTHER INFORMATION: Description of Artificial Sequence: mutant tenth
 69 fibronectin type 3 domain of human fibronectin

71 <220> FEATURE:

72 <221> NAME/KEY: UNSURE

73 <222> LOCATION: (9)

74 <223> OTHER INFORMATION: X at position 9 is either Asn or Lys

76 <400> SEQUENCE: 3

77 Met Gln Val Ser Asp Val Pro Arg Xaa Leu Glu Val Val Ala Ala Thr

78 1 5 10 15

80 Pro Thr Ser Leu Leu Ile Ser Trp Asp Ala Pro Ala Val Thr Val Arg

81 20 25 30

83 Tyr Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln

84 35 40 45

86 Glu Phe Thr Val Pro Gly Ser Lys Ser Thr Ala Thr Ile Ser Gly Leu

87 50 55 60

89 Lys Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Thr Gly Arg

90 65 70 75 80

92 Gly Asp Ser Pro Ala Ser Ser Lys Pro Ile Ser Ile Asn Tyr Arg Thr

93 85 90 95

99 <210> SEQ ID NO: 4

100 <211> LENGTH: 618

101 <212> TYPE: DNA

102 <213> ORGANISM: Artificial Sequence

104 <220> FEATURE:

105 <223> OTHER INFORMATION: Description of Artificial Sequence: B42-FNfn10

106 fusion protein coding region

108 <220> FEATURE:

109 <221> NAME/KEY: unsure

110 <222> LOCATION: (112)..(113)

111 <223> OTHER INFORMATION: N at positions 112 and 113 can be A, C, T, or G

113 <220> FEATURE:

114 <221> NAME/KEY: unsure

115 <222> LOCATION: (115)..(116)

116 <223> OTHER INFORMATION: N at positions 115 and 116 can be A, C, T, or G

118 <220> FEATURE:

119 <221> NAME/KEY: unsure

120 <222> LOCATION: (118)..(119)

121 <223> OTHER INFORMATION: N at positions 118 and 119 can be A, C, T, or G

123 <220> FEATURE:

124 <221> NAME/KEY: unsure

125 <222> LOCATION: (121)..(122)

126 <223> OTHER INFORMATION: N at positions 121 and 122 can be A, C, T, or G

128 <220> FEATURE:

129 <221> NAME/KEY: unsure

130 <222> LOCATION: (124)..(125)

131 <223> OTHER INFORMATION: N at positions 124 and 125 can be A, C, T, or G

133 <220> FEATURE:

134 <221> NAME/KEY: unsure

135 <222> LOCATION: (268)..(269)

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Input Set : A:\U609011.app

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136 <223> OTHER INFORMATION: N at positions 268 and 269 can be A, C, T, or G
138 <220> FEATURE:
139 <221> NAME/KEY: unsure
140 <222> LOCATION: (271)..(272)
141 <223> OTHER INFORMATION: N at positions 271 and 272 can be A, C, T, or G
143 <220> FEATURE:
144 <221> NAME/KEY: unsure
145 <222> LOCATION: (274)..(275) /
146 <223> OTHER INFORMATION: N at positions 274 and 275 can be A, C, T, or G
148 <220> FEATURE:
149 <221> NAME/KEY: unsure
150 <222> LOCATION: (277)..(278)
151 <223> OTHER INFORMATION: N at positions 277 and 278 can be A, C, T, or G
153 <220> FEATURE:
154 <221> NAME/KEY: unsure
155 <222> LOCATION: (280)..(281)
156 <223> OTHER INFORMATION: N at positions 280 and 281 can be A, C, T, or G
158 <220> FEATURE:
159 <221> NAME/KEY: unsure /
160 <222> LOCATION: (283)..(284)
161 <223> OTHER INFORMATION: N at positions 283 and 284 can be A, C, T, or G
163 <220> FEATURE:
164 <221> NAME/KEY: unsure
165 <222> LOCATION: (286)..(287)
166 <223> OTHER INFORMATION: N at positions 286 and 287 can be A, C, T, or G
168 <220> FEATURE:
169 <221> NAME/KEY: unsure
170 <222> LOCATION: (114)
171 <223> OTHER INFORMATION: K at position 114 can be G or T
173 <220> FEATURE:
174 <221> NAME/KEY: unsure /
175 <222> LOCATION: (117)
176 <223> OTHER INFORMATION: K at position 117 can be G or T
178 <220> FEATURE:
179 <221> NAME/KEY: unsure
180 <222> LOCATION: (120)
181 <223> OTHER INFORMATION: K at position 120 can be G or T
183 <220> FEATURE:
184 <221> NAME/KEY: unsure
185 <222> LOCATION: (123)
186 <223> OTHER INFORMATION: K at position 123 can be G or T
188 <220> FEATURE:
189 <221> NAME/KEY: unsure /
190 <222> LOCATION: (126)
191 <223> OTHER INFORMATION: K at position 126 can be G or T
193 <220> FEATURE:
194 <221> NAME/KEY: unsure /
195 <222> LOCATION: (270)
196 <223> OTHER INFORMATION: K at position 270 can be G or T

RAW SEQUENCE LISTING

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Input Set : A:\U609011.app

Output Set: N:\CRF3\05312002\J006760.raw

198 <220> FEATURE:
 199 <221> NAME/KEY: unsure
 200 <222> LOCATION: (273)
 201 <223> OTHER INFORMATION: K at position 273 can be G or T
 203 <220> FEATURE:
 204 <221> NAME/KEY: unsure
 205 <222> LOCATION: (276)
 206 <223> OTHER INFORMATION: K at position 276 can be G or T
 208 <220> FEATURE:
 209 <221> NAME/KEY: unsure
 210 <222> LOCATION: (279)
 211 <223> OTHER INFORMATION: K at position 279 can be G or T
 213 <220> FEATURE:
 214 <221> NAME/KEY: unsure
 215 <222> LOCATION: (282)
 216 <223> OTHER INFORMATION: K at position 282 can be G or T
 218 <220> FEATURE:
 219 <221> NAME/KEY: unsure
 220 <222> LOCATION: (285)
 221 <223> OTHER INFORMATION: K at position 285 can be G or T
 223 <220> FEATURE:
 224 <221> NAME/KEY: unsure
 225 <222> LOCATION: (288)
 226 <223> OTHER INFORMATION: K at position 288 can be G or T
 228 <400> SEQUENCE: 4
 229 atggactaca aggacgacga tgacaagggt atgcagggtt ctgatgttcc gaccgacctg 60
 230 gaagttgttg ctgcgacccc gactagcctg ctgatcagct gggatgctcc tnnknnknnk' 120
 231 nnknnktatt accgtatcac gtacgggtgaa accgggtgga actccccggg tcaggaattc 180
 232 actgtacctg gttccaagtc tactgctacc atcagcggcc tgaaaccggg tgctgactat 240
 233 accatcaactg tatacgtgtg tactggcnnk nnknnknnkn nknnknnknc caagccaatc 300
 234 tcgattaact accgtaccag tggtagcggg gggtcccctc caaaaaagaa gagaaaggta 360
 235 gctggtatca ataaagatat cgaggagtgc aatgccatca ttgagcagtt tatcgactac 420
 236 ctgcgcaccg gacaggagat gccgatggaa atggcggatc aggcgattaa cgtggtgccg 480
 237 ggcattgacg cgaaaaccat tcttcacgcc gggccgccga tccagcctga ctggctgaaa 540
 238 tcgaatggtt ttcattgaaat tgaagcggat gttaacgata ccagcctctt gctgagtgga 600
 239 gattaactcg aggcattgc 618
 242 <210> SEQ ID NO: 5
 243 <211> LENGTH: 201
 244 <212> TYPE: PRT
 245 <213> ORGANISM: Artificial Sequence
 247 <220> FEATURE:
 248 <223> OTHER INFORMATION: Description of Artificial Sequence: artificial
 249 B42-FNfn10 fusion protein
 251 <220> FEATURE:
 252 <221> NAME/KEY: UNSURE
 253 <222> LOCATION: (38)..(42)
 254 <223> OTHER INFORMATION: Xaa at any position can be any amino acid
 256 <220> FEATURE:
 257 <221> NAME/KEY: UNSURE

RAW SEQUENCE LISTING

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Input Set : A:\U609011.app

Output Set: N:\CRF3\05312002\J006760.raw

258 <222> LOCATION: (90)..(96)

259 <223> OTHER INFORMATION: Xaa at any position can be any amino acid

261 <400> SEQUENCE: 5

262 Met Asp Tyr Lys Asp Asp Asp Asp Lys Gly Met Gln Val Ser Asp Val
263 1 5 10 15265 Pro Thr Asp Leu Glu Val Val Ala Ala Thr Pro Thr Ser Leu Leu Ile
266 20 25 30268 Ser Trp Asp Ala Pro Xaa Xaa Xaa Xaa Xaa Tyr Tyr Arg Ile Thr Tyr
269 35 40 45271 Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe Thr Val Pro Gly
272 50 55 60274 Ser Lys Ser Thr Ala Thr Ile Ser Gly Leu Lys Pro Gly Val Asp Tyr
275 65 70 75 80277 Thr Ile Thr Val Tyr Ala Val Thr Gly Xaa Xaa Xaa Xaa Xaa Xaa Xaa
278 85 90 95280 Ser Lys Pro Ile Ser Ile Asn Tyr Arg Thr Ser Gly Thr Gly Gly Ser
281 100 105 110283 Pro Pro Lys Lys Lys Arg Lys Val Ala Gly Ile Asn Lys Asp Ile Glu
284 115 120 125286 Glu Cys Asn Ala Ile Ile Glu Gln Phe Ile Asp Tyr Leu Arg Thr Gly
287 130 135 140289 Gln Glu Met Pro Met Glu Met Ala Asp Gln Ala Ile Asn Val Val Pro
290 145 150 155 160292 Gly Met Thr Pro Lys Thr Ile Leu His Ala Gly Pro Pro Ile Gln Pro
293 165 170 175295 Asp Trp Leu Lys Ser Asn Gly Phe His Glu Ile Glu Ala Asp Val Asn
296 180 185 190298 Asp Thr Ser Leu Leu Leu Ser Gly Asp
299 195 200

302 <210> SEQ ID NO: 6

303 <211> LENGTH: 96

304 <212> TYPE: PRT

305 <213> ORGANISM: Artificial Sequence

307 <220> FEATURE:

308 <223> OTHER INFORMATION: Description of Artificial Sequence: FNfn10
309 polypeptide monobody

311 <220> FEATURE:

312 <221> NAME/KEY: UNSURE

313 <222> LOCATION: (28)..(32)

314 <223> OTHER INFORMATION: Xaa at any position can be any amino acid

316 <220> FEATURE:

317 <221> NAME/KEY: UNSURE

318 <222> LOCATION: (80)..(86)

319 <223> OTHER INFORMATION: Xaa at any position can be any amino acid

321 <400> SEQUENCE: 6

322 Met Gln Val Ser Asp Val Pro Thr Asp Leu Glu Val Val Ala Ala Thr
323 1 5 10 15325 Pro Thr Ser Leu Leu Ile Ser Trp Asp Ala Pro Xaa Xaa Xaa Xaa Xaa
326 20 25 30

RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/10/006,760

DATE: 05/31/2002
TIME: 08:32:23

Input Set : A:\U609011.app
Output Set: N:\CRF3\05312002\J006760.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:3; Xaa Pos. 9
Seq#:4; N Pos. 112,113,115,116,118,119,121,122,124,125,268,269,271,272,274
Seq#:4; N Pos. 275,277,278,280,281,283,284,286,287
Seq#:5; Xaa Pos. 38,39,40,41,42,90,91,92,93,94,95,96
Seq#:6; Xaa Pos. 28,29,30,31,32,80,81,82,83,84,85,86
Seq#:7; N Pos. 409,410,412,413,415,416,418,419,421,422,424,425,427,428
Seq#:8; Xaa Pos. 137,138,139,140,141,142,143
Seq#:9; Xaa Pos. 18,19,20,21,22,23,24
Seq#:10; N Pos. 439,440,442,443,445,446,448,449,451,452,595,596,598,599,601
Seq#:10; N Pos. 602,604,605,607,608,610,611,613,614
Seq#:11; Xaa Pos. 147,148,149,150,151,199,200,201,202,203,204,205
Seq#:12; Xaa Pos. 28,29,30,31,32,80,81,82,83,84,85,86
Seq#:13; N Pos. 595,596,598,599,601,602,604,605,607,608,610,611,613,614,616
Seq#:13; N Pos. 617,619,620,622,623,625,626,628,629,631,632,634,635,637,638
Seq#:13; N Pos. 640,641
Seq#:14; Xaa Pos. 199,200,201,202,203,204,205,206,207,208,209,210,211,212
Seq#:14; Xaa Pos. 213,214
Seq#:15; Xaa Pos. 80,81,82,83,84,85,86,87,88,89,90,91,92,93,94,95
Seq#:20; Xaa Pos. 2,3
Seq#:32; Xaa Pos. 2,3